AMENDMENT

Amendments to the Specification:

Please replace the paragraph on page 4 that begins with "The complete genome sequence ..." with the following amended paragraph:

The complete genome sequence of a several isolates of *C. pneumoniae*, was determined by various institutions {Kalman, S. et al., 1999}; {Read, T. et al., 2000}; {Shirai, M. et al., 2000}; see also ~~http://www.~~tigr.org/tigr-scripts/CMR2/CMRHomePage.spl on the world wide web). Although the two strains AR39 and CWL029 were isolated in the U.S.A. before 1987 and Japan in 1994, respectively, their sequence is to a high degree identical, indicating a divergence in recent human history. In addition to these three *C. pneumoniae* strains, the sequence of two *C. trachomatis* strains {Kalman, S. et al., 1999}; {Read, T. et al., 2000} and that of *C. psittaci* {Read, T. et al., 2003} have been determined.

Please replace the paragraph on page 37 that begins with "Cationic (poly)peptides may also ..." with the following amended paragraph:

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database ~~under the following internet address~~on the world wide web at:

~~http://www.~~bbcm.univ.trieste.it/~tossi/pag2.html

Please replace the paragraph on page 49 that begins with "The prediction of HLA ..." with the following amended paragraph:

The prediction of HLA class I-restricted epitopes within the antigen identified by bacterial display was performed using the program SYFPEITHI as described by {Rammensee, H. et al., 1999}.

(~~http://~~syfpeithi.bmi-heidelberg.com/Scripts/MHCServer.dll/EpPredict.htm)